M. DiBRINO

#15 SK
8/10/00

RAW SEQUENCE LISTING   DATE: 08/03/2000
PATENT APPLICATION: US/09/019,441   TIME: 12:07:00

Input Set : A:\012712-502.app
Output Set: N:\CRF3\08032000\I019441.raw

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          SEQUENCE LISTING
  4  (1) GENERAL INFORMATION:
  6      (i) APPLICANT: REFF, Mitchell E.
  7                     KLOETZER, William S.
  8                     NAKAMURA, Takehiko
 10     (ii) TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
 11                     ANTIBODIES AND USE THEREOF AS THERAPEUTICS
 13    (iii) NUMBER OF SEQUENCES: 35
 15     (iv) CORRESPONDENCE ADDRESS:
 16          (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 17          (B) STREET: P.O. Box 1404
 18          (C) CITY: Alexandria
 19          (D) STATE: Virginia
 20          (E) COUNTRY: United States
 21          (F) ZIP: 22313-1404
 23      (v) COMPUTER READABLE FORM:
 24          (A) MEDIUM TYPE: Floppy disk
 25          (B) COMPUTER: IBM PC compatible
 26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29     (vi) CURRENT APPLICATION DATA:
 30          (A) APPLICATION NUMBER: US/09/019,441
 31          (B) FILING DATE: 05-Feb-1998
 32          (C) CLASSIFICATION:
 34    (vii) PRIOR APPLICATION DATA:
 35          (A) APPLICATION NUMBER: US 08/803,085
 36          (B) FILING DATE: 20-FEB-1997
 38   (viii) ATTORNEY/AGENT INFORMATION:
 39          (A) NAME: Teskin, Robin L.
 40          (B) REGISTRATION NUMBER: 35,030
 41          (C) REFERENCE/DOCKET NUMBER: 012712-502
 43     (ix) TELECOMMUNICATION INFORMATION:
 44          (A) TELEPHONE: (703) 836-6620
 45          (B) TELEFAX: (703) 836-2021
 48  (2) INFORMATION FOR SEQ ID NO: 1:
 50      (i) SEQUENCE CHARACTERISTICS:
 51          (A) LENGTH: 390 base pairs
 52          (B) TYPE: nucleic acid
 53          (C) STRANDEDNESS: single
 54          (D) TOPOLOGY: linear
 56     (ii) MOLECULE TYPE: DNA (genomic)
 58     (ix) FEATURE:
 59          (A) NAME/KEY: CDS
 60          (B) LOCATION: 1..390
 62     (ix) FEATURE:
 63          (A) NAME/KEY: mat_peptide
 64          (B) LOCATION: 58..390
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C--> 30
C--> 31

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67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 ATG GCC TGG ACT CTG CTC CTC GTC ACC CTC CTC ACT CAG GGC ACA GGA          48
70 Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly
71 -19               -15                  -10                    -5
73 TCC TGG GCT CAG TCT GCC CCG ACT CAG CCT CCC TCT GTG TCT GGG TCT          96
74 Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser
75          -1  1              Thr Gln Pro 5         Val Ser Gly 10
77 CCT GGA CAG TCG GTC ACC ATC TCC TGC ACT GGA ACC AGC GAT GAC GTT         144
78 Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
79      15                  20                  25
81 GGT GGT TAT AAC TAT GTC TCC TGG TAC CAA CAC CAC CCA GGC AAA GCC         192
82 Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
83 30                  35                  40                      45
85 CCC AAA CTC ATG ATT TAT GAT GTC GCT AAG CGG GCC TCA GGG GTC TCT         240
86 Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
87                  50                  55                  60
89 GAT CGC TTC TCT GGC TCC AAG TCT GGC AAC ACG GCC TCC CTG ACC ATC         288
90 Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
91              65                  70                  75
93 TCT GGG CTC CAG GCT GAG GAC GAG GCT GAT TAT TAC TGT TGT TCA TAT         336
94 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
95          80                  85                  90
97 ACA ACC AGT AGC ACT TTG TTA TTC GGA AGA GGG ACC CGG TTG ACC GTC         384
98 Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
99      95                  100                 105
101 CTA GGT                                                                390
102 Leu Gly
103 110
106 (2) INFORMATION FOR SEQ ID NO: 2:
108      (i) SEQUENCE CHARACTERISTICS:
109            (A) LENGTH: 423 base pairs
110            (B) TYPE: nucleic acid
111            (C) STRANDEDNESS: single
112            (D) TOPOLOGY: linear
114      (ii) MOLECULE TYPE: DNA (genomic)
117      (ix) FEATURE:
118            (A) NAME/KEY: CDS
119            (B) LOCATION: 1..423
121      (ix) FEATURE:
122            (A) NAME/KEY: mat_peptide
123            (B) LOCATION: 58..423
126      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
128 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG         48
129 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
130 -19              -15                  -10                  -5
132 GTC CTG TCC CAG CTG CAG CTG CAG GAG TCG GGC CCA GGA GTG GTG AAG         96
133 Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
134          -1  1              5                   10
136 CCT TCG GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCT GTC        144
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137 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
138     15                  20                  25
140 AGC AGT AGT AAC TGG TGG ACC TGG ATC CGC CAG CCC CCA GGG AAG GGA      192
141 Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
142     30                  35                  40                  45
144 CTG GAG TGG ATT GGA CGT ATC TCT GGT AGT GGT GGG GCC ACC AAC TAC      240
145 Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
146                 50                  55                  60
148 AAC CCG TCC CTC AAG AGT CGA GTC ATC ATT TCA CAA GAC ACG TCC AAG      288
149 Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
150             65                  70                  75
152 AAC CAG TTC TCC CTG AAC CTG AAC TCT GTG ACC GCC GCG GAC ACG GCC      336
153 Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
154         80                  85                  90
156 GTG TAT TAC TGT GCC AGA GAT TGG GCC CAA ATA GCT GGA ACA ACG CTA      384
157 Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
158         95                  100                 105
160 GGC TTC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA                  423
161 Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
162 110                 115                 120
165 (2) INFORMATION FOR SEQ ID NO: 3:
167     (i) SEQUENCE CHARACTERISTICS:
168         (A) LENGTH: 387 base pairs
169         (B) TYPE: nucleic acid
170         (C) STRANDEDNESS: single
171         (D) TOPOLOGY: linear
173     (ii) MOLECULE TYPE: DNA (genomic)
176     (ix) FEATURE:
177         (A) NAME/KEY: CDS
178         (B) LOCATION: 1..387
180     (ix) FEATURE:
181         (A) NAME/KEY: mat_peptide
182         (B) LOCATION: 67..387
185     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
187 ATG GAC ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTT CTG CTC TGG       48
188 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
189 -22     -20                 -15                 -10
191 CTC CCA GGT GCC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC       96
192 Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
193     -5                  -1  1                   5                  10
195 CTG TCT GCA TCT GTA GGG GAC AGA GTC ACC ATC ACT TGC AGG GCA AGT      144
196 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
197                 15                  20                  25
199 CAG GAC ATT AGG TAT TAT TTA AAT TGG TAT CAG CAG AAA CCA GGA AAA      192
200 Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
201             30                  35                  40
203 GCT CCT AAG CTC CTG ATC TAT GTT GCA TCC AGT TTG CAA AGT GGG GTC      240
204 Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
205             45                  50                  55
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207 CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA GAG TTC ACT CTC ACC        288
208 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
209         60                  65                  70
211 GTC AGC AGC CTG CAG CCT GAA GAT TTT GCG ACT TAT TAC TGT CTA CAG        336
212 Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
213 75                  80                  85                  90
215 GTT TAT AGT ACC CCT CGG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC        384
216 Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
217                 95                  100                 105
219 AAA                                                                    387
220 Lys
224 (2) INFORMATION FOR SEQ ID NO: 4:
226     (i) SEQUENCE CHARACTERISTICS:
227         (A) LENGTH: 411 base pairs
228         (B) TYPE: nucleic acid
229         (C) STRANDEDNESS: single
230         (D) TOPOLOGY: linear
232     (ii) MOLECULE TYPE: DNA (genomic)
235     (ix) FEATURE:
236         (A) NAME/KEY: CDS
237         (B) LOCATION: 1..411
239     (ix) FEATURE:
240         (A) NAME/KEY: mat_peptide
241         (B) LOCATION: 58..411
244     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
246 ATG GAG TTT GGG CTG AGC TGG GTT TTC CTT GTT CCT CTT TTG AAA GGT         48
247 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly
248 -19             -15                 -10                 -5
250 GTC CAG TGT GAG GTG CAG CTG GTG GAG TCT GGG GGC GGC TTG GCA AAG         96
251 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
252         -1  1               5                   10
254 CCT GGG GGG TCC CTG AGA CTC TGG TGC GCA GCC TCC GGG TTC AGG TTC        144
255 Pro Gly Gly Ser Leu Arg Leu Trp Cys Ala Ala Ser Gly Phe Arg Phe
256     15                  20                  25
258 ACC TTC AAT AAC TAC TAC ATG GAC TGG GTC CGC CAG GCT CCA GGG CAG        192
259 Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
260 30                  35                  40                  45
262 GGG CTG GAG TGG GTC TCA CGT ATT AGT AGT AGT GGT GAT CCC ACA TGG        240
263 Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
264                 50                  55                  60
266 TAC GCA GAC TCC GTG AAG GGC AGA TTC ACC ATC TCC AGA GAG AAC GCC        288
267 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
268             65                  70                  75
270 AAC AAC ACA CTG TTT CTT CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG        336
271 Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
272         80                  85                  90
274 GCT GTC TAT TAC TGT GCG AGC TTG ACT ACA GGG TCT GAC TCC TGG GGC        384
275 Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
276     95                  100                 105
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278 CAG GGA GTC CTG GTC ACC GTC TCC TCA                              411
279 Gln Gly Val Leu Val Thr Val Ser Ser
280 110              115
283 (2) INFORMATION FOR SEQ ID NO: 5:
285      (i) SEQUENCE CHARACTERISTICS:
286          (A) LENGTH: 41 base pairs
287          (B) TYPE: nucleic acid
288          (C) STRANDEDNESS: single
289          (D) TOPOLOGY: linear
291     (ii) MOLECULE TYPE: DNA (genomic)
293     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
295 ATCACAGATC TCTCACCATG GACATGAGGG TCCCCGCTCA G                    41
298 (2) INFORMATION FOR SEQ ID NO: 6:
300      (i) SEQUENCE CHARACTERISTICS:
301          (A) LENGTH: 35 base pairs
302          (B) TYPE: nucleic acid
303          (C) STRANDEDNESS: single
304          (D) TOPOLOGY: linear
306     (ii) MOLECULE TYPE: DNA (genomic)
308     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
310 ATCACAGATC TCTCACCATG AGGCTCCCTG CTCAG                           35
313 (2) INFORMATION FOR SEQ ID NO: 7:
315      (i) SEQUENCE CHARACTERISTICS:
316          (A) LENGTH: 35 base pairs
317          (B) TYPE: nucleic acid
318          (C) STRANDEDNESS: single
319          (D) TOPOLOGY: linear
321     (ii) MOLECULE TYPE: DNA (genomic)
324     (ix) FEATURE:
325          (A) NAME/KEY: misc_feature
326          (B) LOCATION: 24
327          (D) OTHER INFORMATION: /note= "Nucleotide 24 is N wherein
328 N = A/G."
330     (ix) FEATURE:
331          (A) NAME/KEY: misc_feature
332          (B) LOCATION: 32
333          (D) OTHER INFORMATION: /note= "Nucleotide 32 is N wherein
334 N = T/G."
336     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
338 ATCACAGATC TCTCACCATG GAANCCCCAG CNCAG                           35
341 (2) INFORMATION FOR SEQ ID NO: 8:
343      (i) SEQUENCE CHARACTERISTICS:
344          (A) LENGTH: 38 base pairs
345          (B) TYPE: nucleic acid
346          (C) STRANDEDNESS: single
347          (D) TOPOLOGY: linear
349     (ii) MOLECULE TYPE: DNA (genomic)
351     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
353 ATCACAGATC TCTCACCATG GTGTTGCAGA CCCAGGTC                        38
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VERIFICATION SUMMARY   DATE: 08/03/2000
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]